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AMSH1 -----MEDHIDVSLSPFEERVRALSKLGCNITISEDITPRR 33
AMSH2 MDQ PFTVNSLKLAAMPDHTDVSLSFEERVRALSKLGCNITISEDITPRR 50
AMSH -----MSDHGDVSLPFEDVRALSQLGS AVEVNEDI PPRR 35
      *.** ****.**,*****;**. : :.***.***

AMSH1 YFRSGVEMERMASVYLEIGHLENAFVLYNKFITLFEVERLPMHRDYQQCAV 85
AMSH2 YFRSGVEMERMASVYLEIGHLENAFVLYNKFITLFEVERLPMHRDYQQCAV 100
AMSH YFRSGVEIIRMASIYSEEGNIEHAFI LYNKYITLFIK LFKHRDYKSAVI 85
      *****; ****,* ****;* **;****;*****;*****;*****;...

AMSH1 FEKQDINKKLKEIAFFPTDELKNDLLKYNVEYQEYLQSKNKYKAEILK 135
AMSH2 FEKQDINKKLKEIAFFPTDELKNDLLKYNVEYQEYLQSKNKYKAEILK 150
AMSH FEKKDITVKRIKEIAFFKAEIKAEILKRYTKYTYNEEKKKAEELARN 135
      *****;*****;*****;****,* ** ** *.** *; :

AMSH1 LEHQRLIEAERKRIAQMROOQLESEQFLFFDQ LKKQELARGQMRSQQTS 185
AMSH2 LEHQRLIEAERKRIAQMROOQLESEQFLFFDQ LKKQELARGQMRSQQTS 200
AMSH MAIQOQLEKEKQ RVAQQROOQLEQEQJHAFEMIRNQLKELERLKIYQEF 185
      : : * *;*****;*****.*** **; :;*** : :; *

AMSH1 G-LSEQIDGSALSCFS--THQNNSLINVFADQPNKSDATNYASHSPFVNR 232
AMSH2 G-LSEQIDGSALSCFS--THQNNSLINVFADQPNKSDATNYASHSPFVNR 247
AMSH GKVDPLGLGOLVPLDLEKPSLDVFFTLTVSSIQPSDCHTTPVPAKPFVDR 235
      * :. :.*. :. :. : : . *. * : **.....* .11.* **

AMSH1 ALTPAATLSAVQNLVVEGLRCVVLPEDLCHKFLQLAESNTVRGIETCGIL 282
AMSH2 ALTPAATLSAVQNLVVEGLRCVVLPEDLCHKFLQLAESNTVRGIETCGIL 297
AMSH SLKPGALSNEESIPTIDGLRHVVVPGRLCPQLQLASANTARGVETCGIL 285
      :*.** . : . .11*** **;* **;*****;**.***;*****

AMSH1 CGKLTENEFTTITHVIVPKQSAGPDYCDMENVEELNVQDQHDLLTLGWI 332
AMSH2 CGKLTENEFTTITHVIVPKQSAGPDYCDMENVEELNVQDQHDLLTLGWI 347
AMSH CGKLTENEFTTITHVLIKQSAGSDYCDTENEELNLIQDQGLITLGI 335
      ****;*****;*****.***; ** ****;***;*****

AMSH1 TPTQTATFLSSVLLHTBCSYQLMLPEAIIVCSFKHDTGIFRLINAGML 382
AMSH2 TPTQTATFLSSVLLHTBCSYQLMLPEAIIVCSFKHDTGIFRLINAGML 397
AMSH TPTQTATFLSSVLLHTBCSYQLMLPESAIVCSFKFQETGFFKLTDEGLE 385
      *;*****;*****;*****;*****.11**;***; :

AMSH1 EVSACKKKGIFHPHTKEPRLFSICKHV--LVKDIKIIVLDIR----- 421
AMSH2 EVSACKKKGIFHPHTKEPRLFSIQKFLSGIISGTALENEPLXIGYGPNGFP 447
AMSH EISSCRQKGIFHPHSDPPLFCSCSHVT--VVDRAVTITDLR----- 424
      *;*****;*** ** . . : : : : *

AMSH1 -----
AMSH2 LLGISRSSSPSEQL 461
AMSH -----

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FIGURE 2

COP9_su5_Hs	VGRLENAIGWYHSHPGYGCWLSGIDVSTQMLNQQFQEPFVA--VVIDPTRTISAGKVNLG
COP9_su5_Dm	VGRMEHAVGWYHSHPGYGCWLSGINVSTQMLNQTYQEPFVA--IVVDPVRTVSAGKVCLG
COP9_su5_At	AGRLENVVGWYHSHPGYGCWLSGIDVSTQRLNQQHQPFLA--VVIDPTRTVSAGKVEIG
COP9_su5_Ce	EGRKEKVVGWYHSHPGYGCWLSGIDVSTQTLNQKFQEPWVA--IVIDPLRTMSAGKVDIG
AF2198_Arcfu	LPICMKVFGTVHSHPSPCRPSEEDLSLFTREGKYHIIVCY--PYDENSWKCYNRKGEEV
PH0451_Pyrho	MPHDESIKGTFFHSHPSFPYPSEGDI MFESKFGGIHIIAAF--PYDEDSVKAFDSEGREV
TVN1035_Thevo	KPIDFSLVGSVHSHPSGITKPSDEDLRMFSLTGKIHIIVGY--PYNLKDYSAYDRSGNKV
MTH971_Metth	LPPFTGAVGSVHSHPGPVNLPSAADLHFFSKNGLFHLLIAH--PYTMETVAAYTRNGDPV
aq_1691_Aquae	ISKGMEIVGVYHSHPDHPDRPSQFDLQRAFPDLSYII FSVQ--KCKVASYSRWELKGDKEF
RV1334_Myctu	EDADEVPVVIYHSHTATEAYPSRTDVKIATEPDAHVVLVSTRDPHRHELRSYRIVDGAVT
RadC_Ecoli	IKINASALIIAHNHPSGCAEPSKADKLITERIIKSCQFMDL--RVLDHIVIGRGEYVSFA
.....	.....HSHP.....S..D

FIGURE 3

COP9_Bu5_Hs	VGRLENAIGWYHSHPGYGCWLSGIDVSTQMLNQOFQEPFVA--VVIDPTRTISAGKVNLG
COP9_Bu5_Dm	VGRMEHAVGWYHSHPGYGCWLSGINVSTQMLNOTYQEPFVA--IVVDPVRTVSAGKVCLG
COP9_Bu5_At	AGRLENVVGWYHSHPGYGCWLSGIDVSTQRLNQOHQEPFLA--VVIDPTRTVSAGKVBIG
COP9_Bu5_Ce	EGEKEKVVGWYHSHPGYGCWLSGIDVSTQTLNQKFQEPWVA--IVIDPLRIMSAGKVDIG
Pad1_Dm	TGRPEMVVGWYHSHPGFGCWLSGVDINTQQSFEALSERAVA--VVVDPIQSVKG-KVVID
Pad1_Hs	TGRPEMVVGWYHSHPGFGCWLSGVDINTQQSFEALSERAVA--VVVDPIQSVKG-KVVID
Sksl_Dd	TGFEDEIVIGWYHSHPGFGCWLSVDVNTQQSFEQLQSRAVA--VVVDPLQSVRG-KVVID
Pad1_Sc	TGRDOMVVGWYHSHPGFGCWLSVDVNTQKSFEQLNSRAVA--VVVDPIQSVKG-KVVID
.....HSHP''''''S'D	

FIGURE 4